

Figure 1

A. Nucleic acid encoding human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:1)

1 TACTGGAAGGTGGCGTGCCCTCCTCTGGCTGGTACC**ATG**CAGCTCCCACT
 51 GGCCCTGTGTCTCGTCTGCCTGCTGGTACACACAGCCTTCCGTGTAGTGG
 101 AGGGCCAGGGGTGGCAGGCGTTCAAGAATGATGCCACGGAAATCATCCCC
 151 GAGCTCGGAGAGTACCCCGAGCCTCCACCGGAGCTGGAGAACACAAGAC
 201 CATGAACCGGGCGGAGAACGGAGGGCGGCCTCCCCACCACCCCTTTGAGA
 251 CCAAAGACGTGTCCGAGTACAGCTGCCGCGAGCTGCACTTCACCCGCTAC
 301 GTGACCGATGGGCCGTGCCGCGAGCGCAAGCCGCTCACCGAGCTGGTGTG
 351 CTCGGCCAGTGGCGCCCGCGCGCCTGCTGCCCAACGCCATCGGCCGCG
 401 GCAAGTGGTGGCGACCTAGTGGGCCCCGACTTCCGCTGCATCCCCGACCGC
 451 TACCGCGCGAGCGCGTGCAGCTGCTGTGTCCCGGTGGTGAGGCGCCGCG
 501 CGCGCGCAAGGTGCGCCTGGTGGCCTCGTGCAAGTGCAAGCGCCTCACCC
 551 GCTTCCACAACCACTCGGAGCTCAAGGACTTCGGGACCGAGGCCGCTCGG
 601 CCGCAGAAGGGCCGGAAGCCGCGGCCCGCGCCCGGAGCGCCAAAGCCAA
 651 CCAGGCCGAGCTGGAGAACGCCTAC**TAG**AGCCCGCCCGCGCCCTCCCCA
 701 CCGGCGGGCGCCCCGGCCCTGAACCGCGCCCCACATTTCTGTCTCTGC
 751 GCGTGGTTT

B. Human Cloaked-2 polypeptide most likely mature form (SEQ ID NO:2)

1 QGWQAFKNDATETIIPELGEYPEPPPELENNKTMNRAENGGRPPHHPFETK
 51 DVSEYS**C**RELHFTRYVTDG**P**CRSAKPVTEL**V**CSGQCGPARLLPNAIGRGK
 101 WWRPSGPDFR**C**IPDRYRAQRVQL**L**CPGGEAPRARKVRLVAS**C**KCKRLTRF
 151 HNQSELKDFGTEAARPQKGRKPRPRARSAKANQAELENAY

C. Human Cloaked-2 polypeptide with signal peptide (SEQ ID NO:5)

1 MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATETIIPELGEYPEPPPEL
 51 ENNKTMNRAENGGRPPHHPFETKDVSEYSCRELHFTRYVTDG**P**CRSAKPV
 101 TELVCSGQCGPARLLPNAIGRGKWWWRPSGPDFR**C**IPDRYRAQRVQL**L**CPG
 151 GEAPRARKVRLVAS**C**KCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRAR
 201 SAKANQAELENAY

10650-124990

Figure 2A. Nucleic acid encoding mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:3)

1 **ATG**CAGCCCTCACTAGCCCCGTCCTCATCTGCCTACTTGTGCACGCTGC
 51 CTTCTGTGCTGTGGAGGGCCAGGGGTGGCAAGCCTTCAGGAATGATGCCA
 101 CAGAGGTCATCCCAGGGCTTGGAGAGTACCCCGAGCCTCCTCCTGAGAAC
 151 AACCAGACCATGAACCGGGCGGAGAATGGAGGCAGACCTCCCCACCATCC
 201 CTATGACGCCAAAGATGTGTCCGAGTACAGCTGCCGCGAGCTGCACTACA
 251 CCCGCTTCCTGACAGACGGCCCATGCCGCAGCGCCAAGCCGGTCACCGAG
 301 TTGGTGTGCTCCGGCCAGTGGCGCCCCGCGCGGCTGCTGCCCAACGCCAT
 351 CGGGCGCGTGAAGTGGTGGCGCCCGAACGGACCGGATTTCGCTGCATCC
 401 CGGATCGCTACCGCGCGCAGCGGGTGCAGCTGCTGTGCCCGGGGGCGCG
 451 GCGCCGCGCTCGCGCAAGGTGCGTCTGGTGGCCTCGTGCAAGTGCAAGCG
 501 CCTCACCCGCTTCCACAACCAAGTCCGAGCTCAAGGACTTCGGGCCGGAGA
 551 CCGCGCGGCGCGAGAAGGGTCGCAAGCGCGGGGGGGGGCGCGCGGGGAGCC
 601 AAAGCCAACCAGGCGGAGCTGGAGAACGCCTAC**TAG**

B. Mouse Cloaked-2 polypeptide most likely mature form (SEQ ID NO:4)

1 QGWQAFRNDATEVIPGLGEYPEPPPENQTMNRAENGGRPPHHPYDAKDV
 51 SEYSCRELHYTRFLTDGPCRSAPVTELVCSGQCGPARLLPNAIGRVKWW
 101 RPNGPDFRCIPDRYRAQRVQLLCPGGAAPRSRKVRLVASCKCKRLTRFHN
 151 QSELKDFGPETARPQKGRKPRPGARGAKANQAELENAY

C. Mouse Cloaked-2 polypeptide with signal peptide (SEQ ID NO:6)

1 MQPSLAPCLICLLVHAAFCAVEGQGWQAFRNDATEVIPGLGEYPEPPPEN
 51 NQTMNRAENGGRPPHHPYDAKDVSEYSCRELHYTRFLTDGPCRSAPVTE
 101 LVCSGQCGPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPGGA
 151 APRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGARGA
 201 KANQAELENAY

T06250-1223850

Figure 3

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GAP of: Human Cloaked-2 check: 5775 from: 1 to: 213
      to: Mouse Cloaked-2 check: 9489 from: 1 to: 211
```

Symbol comparison table:
/GCGDISK/gcg10/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003

```

Quality:      1028      Length:      213
Ratio:        4.872     Gaps:         1
Percent Similarity: 91.469  Percent Identity: 88.152

```

Match display thresholds for the alignment(s):

$$I = \text{IDENTITY}$$
$$: = 2$$

$\rho = 1$

Human Cloaked-2 (SEQ ID NO: 5) x
Mouse Cloaked-2 (SEQ ID NO: 6)

```

1  MQLPLALCLVCLLVHTAFRVVEGQGQWQAFKNDATEIIPELGEYPEPPPEL  50
  ||  ||  ||:|||||  ||  |||||:||||:|  |||||
1  MQPSLAPCLICLLVHAAFCAVEGQGQWQAFRNDATEVIPGLGEYPEPPP..  48

51  ENNKTMNRAENGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAPKV  100
  |||.|||||:|  |||||:|.|||||
49  ENNQTMNRAENGGRPPHHPYDAKDVSSEYSCRELHYTRFLTDGPCRSAPKV  98

101  TELVCSGQCGPARLLPNAIGRGKWWRPSGPDFRCIPDRYRAQRVQLLCPG  150
  |||||  |||||.|||||
99  TELVCSGQCGPARLLPNAIGRVKWWRPNGPDFRCIPDRYRAQRVQLLCPG  148

151  GEAPRARKVRLVASCKCKRLTRFHNQSELKDFGTEAARPQKGRKPRPRAR  200
  |||.|||||  |||||
149  GAAPRSRKVRLVASCKCKRLTRFHNQSELKDFGPETARPQKGRKPRPGAR  198

201  SAKANQAELENAY  213
  |||||
199  GAKANQAELENAY  211

```

Figure 4

```
GAP of: Human Cloaked-1  check: 1888  from: 1  to: 183
      to: Human Cloaked-2  check: 185   from: 1  to: 190
```

Symbol comparison table:
/GCGDISK/gcg10/gcgcore/data/rundata/blosum62.cmp
CompCheck: 6430

Gap Weight:	8	Average Match:	2.912
Length Weight:	2	Average Mismatch:	-2.003

Quality:	335	Length:	196
Ratio:	1.831	Gaps:	6
Percent Similarity:	52.542	Percent Identity:	42.938

Match display thresholds for the alignment(s):

```
| = IDENTITY
: = 2
. = 1
```

Human Cloaked-1 (SEQ ID NO: 25) x
Human Cloaked-2 (SEQ ID NO: 2)

```

1  ....FKNDATEILYSHVVKP.VPAHPSSNSTLNQARNGGRHFSNTGLDR 44
   |||||: | | .| |:|. ||| | . :
1  QGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAENGGRP.PHPFET 49
   . .
45 NTRVQVGCRELRSTKYISDGQCTSISPLKELVCAGECLPLPVLPNWIGGG 94
   : |||| |:|:|. || | | . ||| |:| | . ||| || |
50 KDVSEYSCRELHFTRYVTDGPCRSAPVTELVCSGQCGPARLLPNAIGRG 99
   . .
95 YGTTYWSRRSSQEWRCVNDKTRTQRIQLQCQDG.STRTYKITVVTACKCK 143
   |:| | | :. ||: | | |:| | | . | |: . | . ||||
100 ...KWW.RPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCK 145
   . .
144 RYTRQHNESSHNFESMSPAKPVQHHRRERKRASKSSKHSMS..... 183
   | || ||:| | | : | || |:|. .
146 RLTRFHNQSELKDFGTEAARPQKGRKPRPRA.RSAKANQAELENAY 190

```